

**REMARKS**

**I. Status of the Claims**

Claims 1, 3, 8, 19, and 20 are currently pending under examination.

**II. Claim Rejection: 35 U.S.C. §102(e)**

The Examiner rejected claims under 35 U.S.C. §102(e) for alleged anticipation by Guegler *et al.* (US 2003/0013156). Applicants respectfully traverse the rejection.

To anticipate a pending claim, a prior art reference must provide, either expressly or implicitly, each and every limitation of the pending claim. MPEP §2131. To serve as the basis of a §102(e) rejection, a reference must be either a patent or an application for patent by another filed in the U.S. prior to the invention by the applicant of the application under examination. The pending claims of this application are drawn to a nucleic acid, which comprises the polynucleotide sequence of SEQ ID NO:2 or 3, or encodes for a polypeptide comprising the amino acid sequence of SEQ ID NO:1. SEQ ID NO:3 encodes for SEQ ID NO:1, whereas SEQ ID NO:2 includes SEQ ID NO:3 and additional upstream and downstream non-coding sequences. Both SEQ ID NO:1 and SEQ ID NO:3 are fully and accurately disclosed in USSN 60/226,253 (filed August 17, 2000), to which the instant application claims priority.

The Guegler *et al.* reference, on the other hand, was filed July 31, 2002, as the continuation application of USSN 09/735,932, filed December 14, 2000, claiming priority to USSN 60/211,223, filed June 13, 2000. First, the Examiner asserted that Guegler *et al.* disclose an amino acid sequence (SEQ ID NO:2) that is identical to SEQ ID NO:1 of the instant application. Secondly, the Examiner alleged that USSN 60/211,223 discloses a polynucleotide sequence 100% identical to SEQ ID NO:3 of this application as well as an amino acid sequence identical to SEQ ID NO:1 of this application (page 3 of the Office Action mailed September 29, 2004, and attached copies of Figures 1 and 2 of USSN 60/211,223).

The Examiner is incorrect. To begin with, SEQ ID NO:3 of this application contains 1728 nucleotides and the polynucleotide sequence in Figure 1 of USSN 60/211,223 contains 1743 nucleotides. A closer comparison reveals numerous discrepancies. For instance,

positions 271-285 of SEQ ID NO:3 of this application is GGATTCTTGGAACAG, whereas the corresponding region (positions 271-290) of the sequence found in Figure 1 of USSN 60/211,223 reads GGTCAGATTCTTGGAACAG. Another example of significant differences can be found in the region of approximately 340-360 of the two sequences. See highlighted areas in the attached copies of SEQ ID NO:3 of this application (Exhibit A) and Figure 1 of USSN 60/211,223 (Exhibit B), where yellow indicates identical sequence and orange indicates different sequence. Since the amino acid sequence shown in Figure 2 of USSN 60/211,223 is encoded by the polynucleotide sequence shown in Figure 1, USSN 60/211,223 does not disclose a polynucleotide or amino acid sequence identical to SEQ ID NO:3 or 1 of this application.

Because USSN 60/211,223 does not disclose any polynucleotide or amino acid sequence that is identical to SEQ ID NO:1 or 3 of the present application, this document therefore cannot be relied on as the basis of any anticipation rejection under 35 U.S.C. §102. Even if identical polynucleotide or amino acid sequences are disclosed in the Guegler reference and therefore in USSN 09/735,932, such sequences are entitled only to the priority date of December 14, 2000, when USSN 09/735,932 was filed, but not entitled to the priority date of June 13, 2000, when USSN 60/211,223 was filed. As such, the Guegler reference does not have an effective filing date prior to the constructive date of invention in this application, August 17, 2000, when USSN 60/226,253 was filed. The Guegler reference is therefore not §102(e) prior art to this application.

In view of the forgoing, withdrawal of the anticipation rejection under 35 U.S.C. §102(e) based on the Guegler *et al.* reference is respectfully requested.

Appl. No. 09/927,267  
Amdt. dated December 7, 2004  
Reply to Office Action of September 29, 2004


PATENT

**CONCLUSION**

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

  
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Attachments (Exhibit A: copy of SEQ ID NO:3 of this application; Exhibit B: copy of Figure 1 of USSN 60/211,223)

ASP:cg  
60345773 v1



# Align two sequences

Fri Oct 29 22:00:06 "GMT 2004

```
/usr/tmp/seq1.237717.sca : 2308 nt
>SEQ ID NO:2 018512-006510US, 2308 bases, 69C4C62 2308 nt vs.
>SEQ ID NO:3 018512-006510US, 1728 bases, 1EC170C 1728 nt
scoring matrix: , gap penalties: -12/-2
74.9% identity; Global alignment score: 5732
```

```
10 20 30 40 50 60
/usr/t AGAGGGGAGGAGGAAAACAGAGACAAGACTCAGGCTTCCCTCTGAGGCATGCACCCCCAC
:
SEQ A-----
```

```
70 80 90 100 110 120
/usr/t CTTCTCCAGGGATCTCATTAGAGGTGTTTAGCTGGGCAGGTGTAAGCCCAGGCCCTGGGA
SEQ -----
```

```
130 140 150 160 170 180
/usr/t GACAGGGCAGAGTGCTAGAGCTAGACTGTCTCCACCCCTTCAGTAGCGCTAGCTCTGGTT
SEQ -----
```

```
190 200 210 220 230 240
/usr/t GTGTTGCTAAGAGCCCCAAAGACAAAGAAGTCACAGCAGAAGCCCAACAGCAGCCTCCTT
SEQ -----
```

```
250 260 270 280 290 300
/usr/t CAGACAGTCAGGCACTAGTGCCCAACTCCAGAAGTCCCCTACAGGCAGAGAGGGTGTGGA
SEQ -----
```

```
310 320 330 340 350 360
/usr/t CATCTCACACCCCAGCACCAGACCACAGAACCATGAGCCAGGACACCAAAGTGAAGACAA
:
SEQ -----TGAGCCAGGACACCAAAGTGAAGACAA
10 20
```

```
370 380 390 400 410 420
/usr/t CAGAGTCCAGTCCCCCAGCCCCATCCAAGGCCAGGAAGTTGCTGCCTGTCCTGGACCCAT
:
SEQ CAGAGTCCAGTCCCCCAGCCCCATCCAAGGCCAGGAAGTTGCTGCCTGTCCTGGACCCAT
30 40 50 60 70 80
```

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          430          440          450          460          470          480
/usr/t CTGGGGATTACTACTACTGGTGGCTGAACACAATGGTCTTCCCAGTCATGTATAACCTCA
      :
SEQ    CTGGGGATTACTACTACTGGTGGCTGAACACAATGGTCTTCCCAGTCATGTATAACCTCA
      90          100          110          120          130          140

          490          500          510          520          530          540
/usr/t TCATCCTCGTGTGCAGAGCCTGCTTCCCCGACTTGACAGCACGGTTATCTGGTGGCCTGGT
      :
SEQ    TCATCCTCGTGTGCAGAGCCTGCTTCCCCGACTTGACAGCACGGTTATCTGGTGGCCTGGT
     150          160          170          180          190          200

          550          560          570          580          590          600
/usr/t TGGTGTCTGGACTACACGAGTGACCTGCTATACCTACTAGACATGGTGGTGCCTTCCACA
      :
SEQ    TGGTGTCTGGACTACACGAGTGACCTGCTATACCTACTAGACATGGTGGTGCCTTCCACA
     210          220          230          240          250          260

          610          620          630          640          650          660
/usr/t CAGGATTCTTGGAAACAGGGCATCCTGGTGGTGGACAAGGGTAGGATCTCGAGTCGCTACG
      :
SEQ    CAGGATTCTTGGAAACAGGGCATCCTGGTGGTGGACAAGGGTAGGATCTCGAGTCGCTACG
     270          280          290          300          310          320

          670          680          690          700          710          720
/usr/t TTCGCACCTGGAGTTTCTTCTTGGACCTGGCTTCCCTGATGCCCACAGATGTGGTCTACG
      :
SEQ    TTCGCACCTGGAGTTTCTTCTTGGACCTGGCTTCCCTGATGCCCACAGATGTGGTCTACG
     330          340          350          360          370          380

          730          740          750          760          770          780
/usr/t TGCGGCTGGGCCCCGCACACACCCACCCCTGAGGCTGAACCGCTTTCTCCGCGCGCCCCGCC
      :
SEQ    TGCGGCTGGGCCCCGCACACACCCACCCCTGAGGCTGAACCGCTTTCTCCGCGCGCCCCGCC
     390          400          410          420          430          440

          790          800          810          820          830          840
/usr/t TCTTCGAGGCCTTCGACCGCACAGAGACCCGCACAGCTTACCCAAATGCCTTTCGCATTG
      :
SEQ    TCTTCGAGGCCTTCGACCGCACAGAGACCCGCACAGCTTACCCAAATGCCTTTCGCATTG
     450          460          470          480          490          500

          850          860          870          880          890          900
/usr/t CCAAGCTGATGCTTTACATTTTTGTTCGTCATCCATTGGAACAGCTGCCTATACTTTGCCC
      :
SEQ    CCAAGCTGATGCTTTACATTTTTGTTCGTCATCCATTGGAACAGCTGCCTATACTTTGCCC
     510          520          530          540          550          560

          910          920          930          940          950          960
/usr/t TATCCCGGTACCTGGGCTTCGGGCGTGACGCATGGGTGTACCCGGACCCGCGCAGCCTG
      :
SEQ    TATCCCGGTACCTGGGCTTCGGGCGTGACGCATGGGTGTACCCGGACCCGCGCAGCCTG
     570          580          590          600          610          620

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          970          980          990          1000          1010          1020
/usr/t GCTTTGAGCGCCTGCGGCGCCAGTACCTCTATAGCTTTTACTTCTCCACGCTGATACTGA
      :
      :
      :
SEQ    GCTTTGAGCGCCTGCGGCGCCAGTACCTCTATAGCTTTTACTTCTCCACGCTGATACTGA
      630          640          650          660          670          680

          1030          1040          1050          1060          1070          1080
/usr/t CTACAGTGGGCGATACACCGCCGCCAGCCAGGGAAGAAGAGTACCTCTTCATGGTGGGCG
      :
      :
      :
SEQ    CTACAGTGGGCGATACACCGCCGCCAGCCAGGGAAGAAGAGTACCTCTTCATGGTGGGCG
      690          700          710          720          730          740

          1090          1100          1110          1120          1130          1140
/usr/t ACTTCCTGCTGGCCGTCATGGGTTTCGCCACCATCATGGGTAGCATGAGCTCTGTCTATCT
      :
      :
      :
SEQ    ACTTCCTGCTGGCCGTCATGGGTTTCGCCACCATCATGGGTAGCATGAGCTCTGTCTATCT
      750          760          770          780          790          800

          1150          1160          1170          1180          1190          1200
/usr/t ACAACATGAACACTGCAGATGCGGCTTTCTACCCAGATCATGCACTGGTGAAGAAGTACA
      :
      :
      :
SEQ    ACAACATGAACACTGCAGATGCGGCTTTCTACCCAGATCATGCACTGGTGAAGAAGTACA
      810          820          830          840          850          860

          1210          1220          1230          1240          1250          1260
/usr/t TGAAGCTGCAGCACGTCAACCGCAAGCTGGAGCGGCGAGTTATTGACTGGTATCAGCACC
      :
      :
      :
SEQ    TGAAGCTGCAGCACGTCAACCGCAAGCTGGAGCGGCGAGTTATTGACTGGTATCAGCACC
      870          880          890          900          910          920

          1270          1280          1290          1300          1310          1320
/usr/t TGCAGATCAACAAGAAGATGACCAACGAGGTAGCCATCTTACAGCACTTGCCTGAGCGGC
      :
      :
      :
SEQ    TGCAGATCAACAAGAAGATGACCAACGAGGTAGCCATCTTACAGCACTTGCCTGAGCGGC
      930          940          950          960          970          980

          1330          1340          1350          1360          1370          1380
/usr/t TGCGGGCAGAAGTGGCTGTGTCTGTGCACCTGTCCACTCTGAGCCGGGTGCAGATCTTTC
      :
      :
      :
SEQ    TGCGGGCAGAAGTGGCTGTGTCTGTGCACCTGTCCACTCTGAGCCGGGTGCAGATCTTTC
      990          1000          1010          1020          1030          1040

          1390          1400          1410          1420          1430          1440
/usr/t AGAACTGTGAGGCCAGCCTGCTGGAGGAGCTGGTGCTGAAGCTGCAGCCCCAGACCTACT
      :
      :
      :
SEQ    AGAACTGTGAGGCCAGCCTGCTGGAGGAGCTGGTGCTGAAGCTGCAGCCCCAGACCTACT
      1050          1060          1070          1080          1090          1100

          1450          1460          1470          1480          1490          1500
/usr/t CACCAGGTGAATATGTATGCCGCAAAGGAGACATTGGCCAAGAGATGTACATCATCCGAG
      :
      :
      :
SEQ    CACCAGGTGAATATGTATGCCGCAAAGGAGACATTGGCCAAGAGATGTACATCATCCGAG
      1110          1120          1130          1140          1150          1160

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1510      1520      1530      1540      1550      1560
/usr/t AGGGTCAACTGGCCGTGGTGGCAGATGATGGTATCACACAGTATGCTGTGCTCGGTGCAG
      .....
SEQ    AGGGTCAACTGGCCGTGGTGGCAGATGATGGTATCACACAGTATGCTGTGCTCGGTGCAG
1170      1180      1190      1200      1210      1220

1570      1580      1590      1600      1610      1620
/usr/t GGCTCTACTTTGGGGAGATCAGCATCATCAACATCAAAGGGAACATGTCTGGGAACCGCC
      .....
SEQ    GGCTCTACTTTGGGGAGATCAGCATCATCAACATCAAAGGGAACATGTCTGGGAACCGCC
1230      1240      1250      1260      1270      1280

1630      1640      1650      1660      1670      1680
/usr/t GCACAGCCAACATCAAGAGCCTAGGTTATTTCAGACCTATTCTGCCTGAGCAAGGAGGACC
      .....
SEQ    GCACAGCCAACATCAAGAGCCTAGGTTATTTCAGACCTATTCTGCCTGAGCAAGGAGGACC
1290      1300      1310      1320      1330      1340

1690      1700      1710      1720      1730      1740
/usr/t TGCGGGAGGTGCTGAGCGAGTATCCACAAGCACAGACCATCATGGAGGAGAAAGGACGTG
      .....
SEQ    TGCGGGAGGTGCTGAGCGAGTATCCACAAGCACAGACCATCATGGAGGAGAAAGGACGTG
1350      1360      1370      1380      1390      1400

1750      1760      1770      1780      1790      1800
/usr/t AGATCCTGCTGAAAATGAACAAGTTGGACGTGAATGCTGAGGCAGCTGAGATCGCCCTGC
      .....
SEQ    AGATCCTGCTGAAAATGAACAAGTTGGACGTGAATGCTGAGGCAGCTGAGATCGCCCTGC
1410      1420      1430      1440      1450      1460

1810      1820      1830      1840      1850      1860
/usr/t AGGAGGCCACAGAGTCCCGGCTACGAGGCCTAGACCAGCAGCTGGATGATCTACAGACCA
      .....
SEQ    AGGAGGCCACAGAGTCCCGGCTACGAGGCCTAGACCAGCAGCTGGATGATCTACAGACCA
1470      1480      1490      1500      1510      1520

1870      1880      1890      1900      1910      1920
/usr/t AGTTTGCTCGCCTCCTGGCTGAGCTGGAGTCCAGCGCACTTAAGATTGCTTACCGCATTG
      .....
SEQ    AGTTTGCTCGCCTCCTGGCTGAGCTGGAGTCCAGCGCACTTAAGATTGCTTACCGCATTG
1530      1540      1550      1560      1570      1580

1930      1940      1950      1960      1970      1980
/usr/t AACGGCTGGAGTGGCAGACTCGAGAGTGGCCAATGCCCCGAGGACCTGGCTGAGGCTGATG
      .....
SEQ    AACGGCTGGAGTGGCAGACTCGAGAGTGGCCAATGCCCCGAGGACCTGGCTGAGGCTGATG
1590      1600      1610      1620      1630      1640

1990      2000      2010      2020      2030      2040
/usr/t ACGAGGGTGAGCCTGAGGAGGGAAC'TTCCAAAGATGAAGAGGGCAGGGCCAGCCAGGAGG
      .....
SEQ    ACGAGGGTGAGCCTGAGGAGGGAAC'TTCCAAAGATGAAGAGGGCAGGGCCAGCCAGGAGG
1650      1660      1670      1680      1690      1700

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                2050      2060      2070      2080      2090      2100
/usr/t GACCCCAGGTCCAGAGTGACCCCATCCCATCCCAAGGATTCCCACCTCCTAGTGAATC
      ::::::::::::::::::::
SEQ   GACCCCAGGTCCAGAGTGA-----
      1710      1720

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                2110      2120      2130      2140      2150      2160
/usr/t CAGAGTTGTAGTAAAGCCTAACTGCTGCAACTCTGTCATCCTGTCTGCGAGATCACAGAC
SEQ   -----

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                2170      2180      2190      2200      2210      2220
/usr/t ACAGGAGCGAATTGGTCTGTAGATGCCAGCTAGAGATATAGGAGTTTAAACGCACATTCA
SEQ   -----

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                2230      2240      2250      2260      2270      2280
/usr/t GCCCCCACTTACCAGTACACACACACACACACACACACACATTTGCTCATAGACCTGT
SEQ   -----

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                2290      2300
/usr/t TGGCCCCAAGACTGTGCATTCCATCTAA
SEQ   -----

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60211223.061300

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1  ATGAGCCAGG ACACCAAAGT GAAGACAACA GAGTCCAGTC CCCCAGCCCC
51 ATCCAAGGCC AGGAAGTTGC TGCCTGTCCT GGACCCATCT GGGGATTACT
101 ACTACTGGTG GCTGAACACA ATGGTCTTCC CAGTCATGTA TAACCTCATC
151 ATCCTCGTGT GCAGAGCCTG CTTCCCCGAC TTGCAGCACG GTTATCTGGT
201 GGCCTGGTTG GTGCTGGACT ACACGAGTGA CCTGCTATAC CTACTAGACA
251 TGGTGGTGCG CTTCCACACA GGTGAGATT TTTGGAACAG GGGCATCCTG
301 GGTGGTGGGA CAAGGGGTAA GGATCTCCGA GTTCGCCTAC CTTCCGACCC
351 TGGGAGTTTC TTTCTTGGAC CTGGCTTCTT GATGCCCCACA GATGTGGTCT
401 ACGTGCGGCT GGGCCCGCAC ACACCCACCC TGAGGCTGAA CCGCTTCTC
451 CGCGCGCCCC GCCTCTTCGA GGCCTTCGAC CGCACAGAGA CCCGCACAGC
501 TTACCCAAAT GCCTTTCGCA TTGCCAAGCT GATGCTTTAC ATTTTGTGCG
551 TCATCCATTG GAACAGCTGC CTATACTTG CCCTATCCCG GTACCTGGGC
601 TTCGGGCGTG ACGCATGGGT GTACCCGGAC CCCGCGCAGC CTGGCTTTGA
651 CGCGCTGCGG CGCCAGTACC TCTATAGCTT TTAATTCTCC ACGCTGATAC
701 TGACTACAGT GGGCGATACA CCGCCGCCAG CCAGGGAAGA AGAGTACCTC
751 TTCATGGTGG GCGACTTCCT GCTGGCCGTC ATGGGTTTCG CCACCATCAT
801 GGGTAGCATG AGCTCTGTCA TCTACAACAT GAACACTGCA GATGCGGCTT
851 TCTACCCAGA TCATGCACTG GTGAAGAAGT ACATGAAGCT GCAGGACGTC
901 AACCACAAGC TGGAGCGGCG AGTTATTGAC TGGTATCAGC ACCTGCAGAT
951 CAACAAGAAG ATGACCAACG AGGTAGCCAT CTTACAGCAC TTGCCTGAGC
1001 GGCTGCGGGC AGAAGTGGCT GTGTCTGTGC ACCTGTCCAC TCTGAGCCGG
1051 GTGCAGATCT TTCAGAACTG TGAGGCCAGC CTGCTGGAGG AGCTGGTGCT
1101 GAAGCTGCAG CCCCAGACCT ACTCACCAGG TGAATATGTA TGCCGCAAAG
1151 GAGACATTGG CCAAGAGATG TACATCATCC GAGAGGGTCA ACTGGCCGTG
1201 GTGGCAGATG ATGGTATCAC ACAGTATGCT GTGCTCGGTG CAGGGCTCTA
1251 CTTTGGGGAG ATCAGCATCA TCAACATCAA AGGGAACATG TCTGGGAACC
1301 GCCGCACAGC CAACATCAAG AGCCTAGGTT ATTACAGACCT ATTCTGCCTG
1351 AGCAAGGAGG ACCTGCGGGA GGTGCTGAGC GAGTATCCAC AAGCACAGAC
1401 CATCATGGAG GAGAAAGGAC GTGAGATCCT GCTGAAAATG AACAAAGTTG
1451 ACGTGAATGC TGAGGCAGCT GAGATCGCCC TGCAGGAGGC CACAGAGTCC
1501 CGGCTACGAG GCCTAGACCA GCAGCTGGAT GATCTACAGA CCAAGTTTGC
1551 TCGCTCCTG GCTGAGCTGG AGTCCAGCGC ACTTAAGATT GCTTACCGCA
1601 TTGAACGCTT GGAGTGGCAG ACTCGAGAGT GGCCAATGCC CGAGGACCTG
1651 GCTGAGGCTG ATGACGAGGG TGAGCCTGAG GAGGGAACCT CCAAAGATGA
1701 AGAGGGCAGG GCCAGCCAGG AGGGACCCCC AGGTCCAGAG TGA

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# FEATURES:

Start: 1  
Stop: 1741

# HOMOLOGOUS PROTEINS:

## Top 10 BLAST Hits:

gi 2493746 sp Q64359 CNGX_RAT CYCLIC-NUCLEOTIDE-GATED OLFACTORY...	1039	0.0
gi 2493747 sp Q29441 CNG3_BOVIN CYCLIC-NUCLEOTIDE-GATED CATION ...	580	e-165
gi 7688041 emb CAB89685.1  (AJ243933) cyclic nucleotide-gated c...	577	e-163
gi 2780734 dbj BAA24353.1  (AB002801) cyclic nucleotide-gated c...	576	e-163
gi 399230 sp Q03041 CNG2_BOVIN CYCLIC-NUCLEOTIDE-GATED OLFACTOR...	575	e-163
gi 4826633 emb CAB42891.1  (AJ238239) cyclic nucleotide-gated c...	573	e-162
gi 2493751 sp Q90805 CNG1_CHICK CYCLIC NUCLEOTIDE GATED CHANNEL...	573	e-162
gi 346350 pir  A44842 cGMP-gated ion channel protein - human >g...	570	e-161
gi 479946 pir  S35691 cyclic nucleotide-gated channel protein -...	570	e-161
gi 2493745 sp Q28718 CNG2_RABIT CYCLIC-NUCLEOTIDE-GATED OLFACTO...	570	e-161

## blast to dbEST:

no match

FIGURE 1